

Please substitute the following claim set for the pending claim set.

1-89. (Cancelled)

90. (Previously presented) A method of karyotyping a genome of a test eukaryotic cell, comprising:

sequencing a population of pieces of the genome of the test eukaryotic cell to provide nucleotide sequence of said pieces;

matching, *in silico*, pieces of the genome to genomic locations using the nucleotide sequence of said pieces;

counting the pieces within windows of a selected size throughout the genome to determine number of pieces as a function of genomic location, wherein each window comprises a plurality of genetically clustered pieces;

comparing the number of pieces enumerated within each window for the test eukaryotic cell to the average number of pieces in windows of the selected size throughout the genome to obtain piece densities per window, wherein the piece densities per window represent the karyotype of the genome of the test eukaryotic cell.

91. (Cancelled)

92. (Previously presented) The method of claim 90 wherein the pieces within each of the windows map within 40 kb.

93. (Previously presented) The method of claim 90 wherein the pieces within each of the windows map within 200 kb.

94. (Previously presented) The method of claim 90 wherein the pieces within each of the

windows map within 600 kb.

95. (Previously presented) The method of claim 90 wherein the pieces within each of the windows map within 4 Mb.

96. (Previously presented) The method of claim 90 wherein the pieces are defined by the presence of a *BegI* restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.

97. (Currently amended) The method of claim ~~113~~ 90 further comprising the steps of:
comparing piece densities per window for the test eukaryotic cell to piece densities of a reference eukaryotic cell; and

identifying aneuploidy if (a) pieces of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (b) pieces of one or more sex chromosomes in a male are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (c) pieces of X chromosomes in a female are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 3 or greater or less than 1.5 or relative to a reference female eukaryotic cell at a ratio of 1.5 or greater or less than 0.7.

98. (Previously presented) The method of claim 90 wherein pieces representing less than 15 % of the genome of the eukaryotic cell are sequenced, matched, and counted.

99. (Previously presented) A method of determining differences in copy number of portions of the genome of a test eukaryotic cell, comprising:

sequencing a population of pieces of the genome of the test eukaryotic cell to provide nucleotide sequence of said pieces;

matching, *in silico*, pieces of the genome to genomic locations using the nucleotide sequence of said pieces;

dynamically counting the pieces within a moving window of a selected size to determine number of pieces as a function of genomic location, wherein the window comprises a plurality of genetically clustered pieces;

comparing number of pieces enumerated within the window at a genomic location to an average number of pieces in windows of the selected size throughout the genome to obtain piece density per window, wherein a difference in piece density per window between windows reflects a difference in copy number between portions of the genome.

100. (Previously presented) The method of claim 99 wherein the difference in copy number is due to gain or loss of a whole chromosome.

101. (Previously presented) The method of claim 99 wherein the difference in copy number is due to a gain or loss of a chromosomal arm.

102. (Previously presented) The method of claim 99 wherein the difference in copy number is due to an interstitial amplification.

103. (Previously presented) The method of claim 99 wherein the difference in copy number is due to an interstitial deletion.

104. (Previously presented) The method of claim 99 wherein the pieces within the window map within 40 kb.

105. (Previously presented) The method of claim 99 wherein the pieces within the window map within 200 kb.

106. (Previously presented) The method of claim 99 wherein the pieces within the window map within 600 kb.

107. (Previously presented) The method of claim 99 wherein the pieces within the window map within 4 Mb.

108. (Previously Presented) The method of claim 99 wherein the pieces are defined by the presence of a BcgI restriction endonuclease recognition site which is flanked by 12 nucleotides on either end.

109. (Currently amended) The method of claim ~~113~~ 99 further comprising the steps of:

comparing piece densities per window for the test eukaryotic cell to piece densities of a reference eukaryotic cell; and

identifying aneuploidy if (a) pieces of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (b) pieces of one or more sex chromosomes in a male are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 1.5 or greater or less than 0.7; or (c) pieces of X chromosomes in a female are determined to be present in the test eukaryotic cell relative to a reference male eukaryotic cell at a ratio of 3 or greater or less than 1.5 or relative to a reference female eukaryotic cell at a ratio of 1.5 or greater or less than 0.7.

110. (Previously presented) The method of claim 99 wherein pieces representing less than 15 % of the genome of the eukaryotic cell are sequenced, matched, and dynamically counted.

111. (Previously presented) The method of claim 90 or 99 wherein the sequencing is performed by automated nucleotide sequence determination.
112. (Previously presented) The method of claim 90 or 99 wherein between 100,000 and 1,000,000 pieces are sequenced and matched.
113. (Previously presented) The method of claim 90 or 99 further comprising the step of: comparing piece densities per window for the test eukaryotic cell to piece densities of a reference eukaryotic cell.
114. (Previously presented) The method of claim 90 or 99 wherein the selected size is less than or equal to 40 kb.
115. (Previously presented) The method of claim 90 or 99 wherein the selected size is less than or equal to 200 kb.
116. (Previously presented) The method of claim 90 or 99 wherein the selected size is less than or equal to 600 kb.
117. (Previously presented) The method of claim 90 or 99 wherein the selected size is less than or equal to 4 Mb.